

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/211,755

DATE: 12/30/98
TIME: 12:46:10

INPUT SET: S30470.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Jones, Kenneth A.
6 Laz, Thomas M.
7 Borowsky, Beth
8
9 (ii) TITLE OF INVENTION: DNA Encoding a GABABR2 Polypeptide And
10 Uses Thereof
11
12 (iii) NUMBER OF SEQUENCES: 47
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Cooper & Dunham LLP
16 (B) STREET: 1185 Avenue of the Americas
17 (C) CITY: New York
18 (D) STATE: New York
19 (E) COUNTRY: U.S.A.
20 (F) ZIP: 10036
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: Not Yet Known
30 (B) FILING DATE: Herewith
31 (C) CLASSIFICATION:
32
33 (viii) ATTORNEY/AGENT INFORMATION:
34 (A) NAME: White Esq., John P.
35 (B) REGISTRATION NUMBER: 28,678
36 (C) REFERENCE/DOCKET NUMBER: 54002-D
37
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: 212-278-0400
40 (B) TELEFAX: 212-391-0525
41
42 (2) INFORMATION FOR SEQ ID NO:1:
43
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 3244 base pairs
46 (B) TYPE: nucleic acid

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/211,755DATE: 12/30/98
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47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: linear
49
50 (ii) MOLECULE TYPE: DNA (genomic)
51
52 (iii) HYPOTHETICAL: NO
53
54 (iv) ANTI-SENSE: NO
55
56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
57
58 TGACCTCGGG GCAGGTCTTG GTGCAGAGCG TCGCCAAGGA CGCCGAGAGG GAGGCGGGAT 60
59
60 TGCCCAGACA TCCTTCAGCG AAGTGCATGT GTGTTTGTA ACCATCGTTG GCTGTCGGGA 120
61
62 GACCGCGAGG ACCGGTCCAG GCTGCGGCGG AGTCGAGGGC GAGGGAGAGG CCGCGTGAGT 180
63
64 GAGCAGAGTC CAGAGCCGTG CGCCCCAGA ACTGCGCGTC CGCCCCGTGC ACCCCGCGC 240
65
66 GCCATGCCCA GTTGCCCCGC GCGCTCTGCT ACGGGCCCCG TCTCCATCAT GGGCCTCATG 300
67
68 CCGCTCACCA AGGAGGTGGC CAAGGGCAGC ATCGGGCGCG GTGTGCTCCC CGCCGTGGAA 360
69
70 CTGGCCATCG AGCAGATCCG CAACGAGTCA CTCCTGCGCC CCTACTTCCT CGACCTGCGG 420
71
72 CTCTATGACA CGGAGTGCGA CAACGCAAAA GGGTTGAAAG CCTTCTACGA TCGGATAAAA 480
73
74 TACGGGCCGA ACCACTTGAT GGTGTTTGGA GGCGTCTGTC CATCCGTCAC ATCCATCATT 540
75
76 GCAGAGTCCC TCCAAGGCTG GAATCTGGTG CAGCTTTCTT TTGCTGCAAC CACGCCTGTT 600
77
78 CTAGCCGATA AGAAAAATA CCCTTATTTT TTTCGGACCG TCCCATCAGA CAATGCGGTG 660
79
80 AATCCAGCCA TTCTGAAGTT GCTCAAGCAC TACCAGTGGA AGCGCGTGGG CACGCTGACG 720
81
82 CAAGACGTTT AGAGGTTCTC TGAGGTGCGG AATGACCTGA CTGGAGTTCT GTATGGCGAG 780
83
84 GACATTGAGA TTTCAGACAC CGAGAGCTTC TCCAACGATC CCTGTACCAG TGTCAAAAAG 840
85
86 CTGAAGGGGA ATGATGTGCG GATCATCCTT GGCCAGTTTG ACCAGAATAT GGCAGCAAAA 900
87
88 GTGTTCTGTT GTGCATACGA GGAGAACATG TATGGTAGTA AATATCAGTG GATCATTCCG 960
89
90 GGCTGGTACG AGCCTTCTTG GTGGGAGCAG GTGCACACGG AAGCCAATC ATCCCGCTGC 1020
91
92 CTCCGGAAGA ATCTGCTTGC TGCCATGGAG GGCTACATTG GCGTGGATTT CGAGCCCCTG 1080
93
94 AGCTCCAAGC AGATCAAGAC CATCTCAGGA AAGACTCCAC AGCAGTATGA GAGAGAGTAC 1140
95
96 AACACAAGC GGTCAGGCGT GGGGCCCAGC AAGTTCCACG GGTACGCCTA CGATGGCATC 1200
97
98 TGGGTCATCG CCAAGACACT GCAGAGGGCC ATGGAGACAC TGCATGCCAG CAGCCGGCAC 1260
99

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102	ATGAACGAGA	CCAAC'TTCTT	CGGGGTCACG	GGTCAAGTTG	TATTCCGGAA	TGGGGAGAGA	1380
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104	ATGGGGACCA	TTAAATTTAC	TCAATTTCAA	GACAGCAGGG	AGGTGAAGGT	GGGAGAGTAC	1440
105							
106	AACGCTGTGG	CCGACACACT	GGAGATCATC	AATGACACCA	TCAGGTTCCA	AGGATCCGAA	1500
107							
108	CCACCAAAAG	ACAAGACCAT	CATCCTGGAG	CAGCTGCGGA	AGATCTCCCT	ACCTCTCTAC	1560
109							
110	AGCATCCTCT	CTGCCCTCAC	CATCCTCGGG	ATGATCATGG	CCAGTGCTTT	TCTCTTCTTC	1620
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112	AACATCAAGA	ACCGGAATCA	GAAGCTCATA	AAGATGTCGA	GTCCATACAT	GAACAACCTT	1680
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114	ATCATCCTTG	GAGGGATGCT	TTCCTATGCT	TCCATATTTT	TCTTTGGCCT	TGATGGATCC	1740
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116	TTTGTCTCTG	AAAAGACCTT	TGAAACACTT	TGCACCGTCA	GGACCTGGAT	TCTCACCGTG	1800
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118	GGCTACACGA	CCGCTTTTGG	GGCCATGTTT	GCAAAGACCT	GGAGAGTCCA	CGCCATCTTC	1860
119							
120	AAAAATGTGA	AAATGAAGAA	GAAGATCATC	AAGGACCAGA	AACTGC'TTGT	GATCGTGGGG	1920
121							
122	GGCATGCTGC	TGATCGACCT	GTGTATCCTG	ATCTGCTGGC	AGGCTGTGGA	CCCCCTGCGA	1980
123							
124	AGGACAGTGG	AGAAGTACAG	CATGGAGCCG	GACCCAGCAG	GACGGGATAT	CTCCATCCGC	2040
125							
126	CCTCTCCTGG	AGCACTGTGA	GAACACCCAT	ATGACCATCT	GGCTTGGCAT	CGTCTATGCC	2100
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128	TACAAGGGAC	TTCTCATGTT	GTTCGGTTGT	TTCTTAGCTT	GGGAGACCCG	CAACGTCAGC	2160
129							
130	ATCCCCGCAC	TCAACGACAG	CAAGTACATC	GGGATGAGTG	TCTACAACGT	GGGGATCATG	2220
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132	TGCATCATCG	GGGCCGCTGT	CTCCTTCCTG	ACCCGGGACC	AGCCCAATGT	GCAGTTCCTGC	2280
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134	ATCGTGGCTC	TGGTCATCAT	CTTCTGCAGC	ACCATCACCC	TCTGCCTGGT	ATTCTGTCCG	2340
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136	AAGCTCATCA	CCCTGAGAAC	AAACCCAGAT	GCAGCAACGC	AGAACAGGCG	ATTCCAGTTC	2400
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138	ACTCAGAATC	AGAAGAAAGA	AGATTCTAAA	ACGTCCACCT	CGGTCACCAG	TGTGAACCAA	2460
139							
140	GCCAGCACAT	CCCGCCTGGA	GGGCCTACAG	TCAGAAAACC	ATCGCCTGCG	AATGAAGATC	2520
141							
142	ACAGAGCTGG	ATAAAGACTT	GGAAGAGGTC	ACCATGCAGC	TGCAGGACAC	ACCAGAAAAG	2580
143							
144	ACCACCTACA	TTAAACAGAA	CCACTACCAA	GAGCTCAATG	ACATCCTCAA	CCTGGGAAAC	2640
145							
146	TTCACTGAGA	GCACAGATGG	AGGAAAGGCC	ATTTTAAAAA	ATCACCTCGA	TCAAAATCCC	2700
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148	CAGCTACAGT	GGAACACAAC	AGAGCCCTCT	CGAACATGCA	AAGATCCTAT	AGAAGATATA	2760
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150	AACTCTCCAG	AACACATCCA	GCGTCGGCTG	TCCCTCCAGC	TCCCCATCCT	CCACCACGCC	2820
151							
152	TACCTCCCAT	CCATCGGAGG	CGTGGACGCC	AGCTGTGTCA	GCCCCTGCGT	CAGCCCCACC	2880

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153
154 GCCAGCCCCC GCCACAGACA TGTGCCACCC TCCTTCCGAG TCATGGTCTC GGGCCTGTAA      2940
155
156 GGGTGGGAGG CCTGGGCCCC GGGCCTCCCC CGTGACAGAA CCACACTGGG CAGAGGGGTC      3000
157
158 TGCTGCAGAA AACTGTCTGG CTCTGGCTGC GGAGAAGCTG GGCACCATGG CTGGCCTCTC      3060
159
160 AGGACCACTC GGATGGCACT CAGGTGGACA GGACGGGGCA GGGGGAGACT TGGCACCTGA      3120
161
162 CCTCGAGCCT TATTGTGAA GTCCTTATTT CTTCAAAAG AAGAGGAACG GAAATGGGAC      3180
163
164 GTCTTCCTTA ACATCTGCAA ACAAGGAGGC GCTGGGATAT CAAACTTGCA AAAAAAAAAA      3240
165
166 AAAA                                     3244

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 898 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Pro Ser Cys Pro Ala Arg Ser Ala Thr Gly Pro Leu Ser Ile Met
1           5           10           15

Gly Leu Met Pro Leu Thr Lys Glu Val Ala Lys Gly Ser Ile Gly Arg
20           25           30

Gly Val Leu Pro Ala Val Glu Leu Ala Ile Glu Gln Ile Arg Asn Glu
35           40           45

Ser Leu Leu Arg Pro Tyr Phe Leu Asp Leu Arg Leu Tyr Asp Thr Glu
50           55           60

Cys Asp Asn Ala Lys Gly Leu Lys Ala Phe Tyr Asp Ala Ile Lys Tyr
65           70           75           80

Gly Pro Asn His Leu Met Val Phe Gly Gly Val Cys Pro Ser Val Thr
85           90           95

Ser Ile Ile Ala Glu Ser Leu Gln Gly Trp Asn Leu Val Gln Leu Ser
100          105          110

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206	Phe	Ala	Ala	Thr	Thr	Pro	Val	Leu	Ala	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr
207			115					120						125		
208																
209	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Asn	Ala	Val	Asn	Pro	Ala	Ile	Leu
210			130					135					140			
211																
212	Lys	Leu	Leu	Lys	His	Tyr	Gln	Trp	Lys	Arg	Val	Gly	Thr	Leu	Thr	Gln
213		145					150				155					160
214																
215	Asp	Val	Gln	Arg	Phe	Ser	Glu	Val	Arg	Asn	Asp	Leu	Thr	Gly	Val	Leu
216					165					170					175	
217																
218	Tyr	Gly	Glu	Asp	Ile	Glu	Ile	Ser	Asp	Thr	Glu	Ser	Phe	Ser	Asn	Asp
219				180					185					190		
220																
221	Pro	Cys	Thr	Ser	Val	Lys	Lys	Leu	Lys	Gly	Asn	Asp	Val	Arg	Ile	Ile
222			195					200					205			
223																
224	Leu	Gly	Gln	Phe	Asp	Gln	Asn	Met	Ala	Ala	Lys	Val	Phe	Cys	Cys	Ala
225		210					215					220				
226																
227	Tyr	Glu	Glu	Asn	Met	Tyr	Gly	Ser	Lys	Tyr	Gln	Trp	Ile	Ile	Pro	Gly
228		225				230					235				240	
229																
230	Trp	Tyr	Glu	Pro	Ser	Trp	Trp	Glu	Gln	Val	His	Thr	Glu	Ala	Asn	Ser
231					245					250					255	
232																
233	Ser	Arg	Cys	Leu	Arg	Lys	Asn	Leu	Leu	Ala	Ala	Met	Glu	Gly	Tyr	Ile
234				260				265					270			
235																
236	Gly	Val	Asp	Phe	Glu	Pro	Leu	Ser	Ser	Lys	Gln	Ile	Lys	Thr	Ile	Ser
237			275					280					285			
238																
239	Gly	Lys	Thr	Pro	Gln	Gln	Tyr	Glu	Arg	Glu	Tyr	Asn	Asn	Lys	Arg	Ser
240		290					295					300				
241																
242	Gly	Val	Gly	Pro	Ser	Lys	Phe	His	Gly	Tyr	Ala	Tyr	Asp	Gly	Ile	Trp
243		305				310					315				320	
244																
245	Val	Ile	Ala	Lys	Thr	Leu	Gln	Arg	Ala	Met	Glu	Thr	Leu	His	Ala	Ser
246					325					330				335		
247																
248	Ser	Arg	His	Gln	Arg	Ile	Gln	Asp	Phe	Asn	Tyr	Thr	Asp	His	Thr	Leu
249				340					345					350		
250																
251	Gly	Arg	Ile	Ile	Leu	Asn	Ala	Met	Asn	Glu	Thr	Asn	Phe	Phe	Gly	Val
252			355					360					365			
253																
254	Thr	Gly	Gln	Val	Val	Phe	Arg	Asn	Gly	Glu	Arg	Met	Gly	Thr	Ile	Lys
255		370					375					380				
256																
257	Phe	Thr	Gln	Phe	Gln	Asp	Ser	Arg	Glu	Val	Lys	Val	Gly	Glu	Tyr	Asn
258		385				390					395				400	

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/211,755

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TIME: 12:46:14

INPUT SET: S30470.raw

Line	Error	Original Text
29	Wrong application Serial Number	(A) APPLICATION NUMBER: Not Yet Known